OM nucleic - nucleic search, using sw model

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Run on: September 1, 2000, 01:15:48 ; Search time 261.02 Seconds
(without alignments)
4326.089 Million cell updates/sec

Title: US-09-171-553-3
Perfect score: 8209
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

t	Score	Query Match %	Length	DB	ID	Description
1	2244.4	27.3	8535	5	US-08-716-351A-1	Sequence 1, Appl1
2	1747	21.3	8323	4	US-08-110-300A-8	Sequence 8, Appl1
3	1747	21.3	8323	4	US-08-886-642-8	Sequence 8, Appl1
4	1738.4	21.2	8202	2	PCT-US93-08041-8	Sequence 8, Appl1
5	1687.4	20.6	8332	5	US-08-258-420-13	Sequence 13, Appl1
6	1596	19.4	10367	4	US-08-850-961-1	Sequence 1, Appl1
7	1596	19.4	10367	4	US-08-110-300A-9	Sequence 9, Appl1
8	1596	19.4	10367	4	US-08-886-642-9	Sequence 9, Appl1
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10	1596	19.4	10367	5	US-08-105-483-324	Sequence 324, App
11	852.6	10.4	3674	2	US-08-709-209-324	Sequence 324, App
12	852.6	10.4	3674	3	US-08-458-101-324	Sequence 324, App
13	815.4	9.9	6363	4	US-08-929-967-6	Sequence 6, Appl1
14	359.4	4.4	10970	5	US-08-716-351A-5	Sequence 5, Appl1
15	303.8	3.7	1965	2	US-08-258-420-9	Sequence 9, Appl1
16	301.4	3.7	2499	2	US-08-105-483-310	Sequence 310, App
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44	149.6	1.8	1158	5	US-08-691-563C-1	Sequence 1, Appl1
45	144.4	1.8	9661	5	US-08-716-351A-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-716-351A-1
Sequence 1, Application US/08716351A
Patent No. 6033905
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Gibbon Ape Leukemia Virus-Based
TITLE OF INVENTION: Retroviral Vectors
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,351A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03784
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian,, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 15280-128-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8535 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..8535
OTHER INFORMATION: /standard_name= "GalV SEATO Genome"
US-08-716-351A-1

Query Match 27.3%; Score 2244.4; DB 5; Length 8535;
Best Local Similarity 59.1%; Pred. No. 0;
Matches 4366; Conservative 0; Mismatches 2811; Indels 215; Gaps 22;

Qy 332 agcagacgtgctaggaggaatcaaggctgccacctgggggacgcccggaggtgggga 391

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RESULT 2
US-08-110-300A-8

Sequence 8, Application US/08110300A
Patent No. 5643756

GENERAL INFORMATION:
    APPLICANT: Pinter, Abraham
    APPLICANT: Kayman, Samuel
    TITLE OF INVENTION: FUSION GLYCOPROTEINS
    NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Davis Hoxie Faithfull and Hapgood
    STREET: 45 Rockefeller Pl.
    CITY: New York
    STATE: New York
    COUNTRY: USA
    ZIP: 10111

COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/110,300A
    FILING DATE: 20-AUG-1993
    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
    NAME: Jacobs, Seth H.
    REGISTRATION NUMBER: 32,140
    REFERENCE/DOCKET NUMBER: 11698A50
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 212-757-2200
    TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 8:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 8323 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    HYPOTHETICAL: NO
    ANTI-SENSE: NO
US-08-110-300A-8

Query Match
Best Local Similarity   21.38;   Score 1747;   DB 1;   Length 8323;
                         55.6%;   Pred. No. 0;
Matches 4058; Conservative 0; Mismatches 3005; Indels 238; Gaps 27;

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GenCore version 4.5
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Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	% Query Match	Match Length	DB	DB ID	Description
1	1088	32.8	8535	5	US-08-716-351A-1	Sequence 1, Appl
2	933.6	28.1	8323	4	US-08-110-300A-8	Sequence 8, Appl
3	933.6	28.1	8323	4	US-08-886-642-8	Sequence 8, Appl
4	933.6	28.1	8323	6	PCT-US93-08041-8	Sequence 8, Appl
5	932	28.1	10367	1	US-08-110-300A-9	Sequence 9, Appl
6	932	28.1	10357	4	US-08-886-642-9	Sequence 9, Appl
7	932	28.1	10357	6	PCT-US93-08041-9	Sequence 9, Appl
8	916.2	28.1	8332	5	US-08-850-961-1	Sequence 1, Appl
9	910.8	27.4	8202	2	US-08-258-420-13	Sequence 13, Appl
10	624.6	18.8	6363	5	US-08-929-967-6	Sequence 6, Appl
11	300.4	9.0	949	6	PCT-US91-08254-1	Sequence 2, Appl
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13	233	7.0	735	2	US-08-798-000-3	Sequence 3, Appl
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17	218	6.6	3674	2	US-08-709-209-324	Sequence 324, App
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22	119.2	3.6	1158	2	US-08-471-724-1	Sequence 1, Appl
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24	119.2	3.6	1158	3	US-08-384-137-1	Sequence 1, Appl
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27	119.2	3.6	2391	5	US-08-691-563C-57	Sequence 57, Appl
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29	91	2.7	246240	3	US-08-724-394A-21	Sequence 21, Appl
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37	74.8	2.2	645	3	US-08-471-724-8	Sequence 8, Appl
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42	63	1.9	374	2	US-08-686-878A-47	Sequence 47, Appl
43	63	1.9	374	2	US-08-721-489-1	Sequence 1, Appl
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45	53.2	1.6	7218	1	US-08-232-463-14	Sequence 14, Appl

RESULT 1
US-08-716-351A-1
Sequence 1, Application US/08716351A
Patent No. 6033905
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Gibbon Ape Leukemia Virus-Based
TITLE OF INVENTION: Retroviral Vectors
NUMBER OF SEQUENCES: 5
COMPUTER READABLE INFORMATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03784
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian,, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 15280-128-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8535 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..8535
OTHER INFORMATION: /standard_name= "GaLV SEATO Genome"
US-08-716-351A-1

ALIGNMENTS

Query Match 32.8%; Score 1088; DB 5; Length 8535;
Best Local Similarity 63.8%; Pred. No. 0;
Matches 1761; Conservative 0; Mismatches 920; Indels 81; Gaps 4;

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Qy     82 agagatccaggtacgggaagaaccgggcagctcacctggacccgactgccccaagggttc 141
          | ||| ||||  |  || |  || || ||||| ||||||||| || || || |||||||||
Db   3431 AAAGACCCAGAAAAAGGTAACACAGGTCAGCTGACCTGGACGCGGCTACCACAAGGGTTC 3490

Qy    142 aagaactccccgaccatctttgacgaagccctacacagggacctggccaacttcaggatc 201
          |||||||| || ||  |||| ||||| ||||| || ||| | ||    ||||   ||| |||  |
Db   3491 AAGAACTCTCCCACTCTCTTCGACGAGGCCCTCCACCGAGATTTGGCTCCCTTTAGGGCC 3550

Qy    202 caacaccctcaggtgaccctcctccagtacgtggatgacctgcttctggcgggagccacc 261
          |   |||| ||||||    | ||||| || ||||| |||||  |  |  |||| |   ||||
Db   3551 CTCAACCCCCAGGTGGTGTTACTCCAATATGTGGACGACCTCTTGGTGGCCGCCCCCACA 3610

Qy    262 aaacaggactgcttagaaggtacgaaggcactactgctggaattgtctgacctaggctac 321
           |  | ||||||  | |||| ||  ||   ||  | | || | ||   | |   | || |||
Db   3611 TATGAAGACTGCAAAAAAGGAACACAGAAGCTCTTACAGGAGTTAAGTAAGTTGGGGTAC 3670

Qy    322 agagcctctgctaagaaggcccagatttgcaggagagaggtaacatacttggggtacagt 381
           | |  || ||||||||||||||| | |||  |||||| || || ||  ||  |||||||
Db   3671 CGGGTATCGGCTAAGAAGGCCCAGCTCTGCCAGAGAGAAGTCACCTATCTGGGGTACCTA 3730

Qy    382 ttgcggggcgggcagcgatggctgacggaggcacggaagaaaactgtagtccagataccg 441
           |   ||  ||  |  ||||||| ||    || || |||   |||||  |  | || ||
Db   3731 CTCAAGGAAGGAAAAAGATGGCTAACCCCAGCCCGAAAGGCTACTGTTATGAAAATCCCT 3790

Qy    442 gccccaaccacagccaaacaagtgagagagtttttggggacagctggattttgcagactg 501
          |  || || ||  ||| ||| ||  | || ||| | || || || |||||| ||||| ||
Db   3791 GTTCCTACGACCCCCAGACAGGTCCGTGAATTTCTAGGCACTGCCGGATTCTGCAGGCTC 3850

Qy    502 tggatcccggggtttgcgaccttagcagccccactctacccgctaaccaaagaaaaaggg 561
          |||||||| ||||||||  || | || || ||||  | |||||| ||||| |||| |
Db   3851 TGGATCCCTGGGTTTGCTTCCCTGGCTGCACCCTTGTACCCCCTAACAAAAGAGAGCATC 3910

Qy    562 ggattctcctgggctcctgagcaccagaaggcatttgatgctatcaaaaaggccctgctg 621
             ||    ||| ||   || || ||| ||||| |||||    || ||||| ||| |||||
Db   3911 CCTTTTATTTGGACTGAGGAACATCAGCAGGCTTTTGACCACATAAAAAAAGCCTTGCTG 3970

Qy    622 agcgcacctgctctggccctccctgacgtaactaaaccctttacccttta tgtggatgag 681
             || |||||  |||||||||||| ||| | || || || || || || ||| | ||||||
Db   3971 TCAGCCCCTGCATTGGCCCTCCCAGACCTCACCAAGCCATTCACTCTATATATAGATGAG 4030

Qy    682 cgtaagggaggtagcccgaggagttttaacccaaaccctaggaccatggaggagacctgtt 741
           |    || || ||||| |||||  | || || ||  ||||||| ||| || | || || 
Db   4031 AGAGCCGGCGTGGCCCGGGGAGTGCTCACTCAGACTTTAGGACCCTGGCGGCGGCCAGTA 4090

Qy    742 gcctacctgtcaaagaagcttgatcctgtagccagtggttggcccgtatgtctgaaggct 801
          || || || ||||| || || ||||| || ||||| || |||||    || ||||| || 
Db   4091 GCATATCTATCAAAAAAACTGGATCCGGTGGCCAGCGGGTGGCCAACCTGCCTGAAAGCG 4150

Qy    802 atcgcagctgtggccatactggtcaaggacgctgacaaattgactttgggacagaatata 861
           | ||||| || ||  | ||  |||| |||||||||| || || || ||||||||| ||| | 
Db   4151 GTTGCAGCAGTAGCACTCCTTCTCAAAGACGCTGATAAGTTAACCTTGGGACAAAATGTG 4210

Qy    862 actgtaatagccccccatgcattggagaacatcgttcggcagcccccagaccgatggatg 921
          ||||| || ||  |||||    | || | |||||| |||||| ||||| ||||| ||||||
Db   4211 ACTGTGATTGCTTCCCATAGCCTCGAAAGCATCGTGCGGCAACCCCCCGACCGGTGGATG 4270

Qy    922 accaacgcccgcatgacccactatcaaagcctgcttctcacagagagggtcactttcgct 981
          ||||| ||| | ||||| || || || |||||||||  | |   || |||||  | || || 
Db   4271 ACCAATGCCAGAATGACTCATTACCAGAGCCTGCTGTTAAATGAAAGGGTATCGTTTGCG 4330

Qy    982 ccaccagccgctctcaaccctgccactcttctgcctgaagagactgatgaaccagtgact 1041
          || || || |  || ||||| || || || || || |  || | || | |   |       
Db   4331 CCCCCTGCTGTCCTAAACCCAGCTACCCTACTTCCAGTCGAGTCGGAAGCCACCCCAGTG 4390

Qy   1042 catgattgccatcaactattgattgaggagactggggtccgcaaggaccttacagacata 1101
          ||    |||    || |  |    || || |||||    ||    |||||   ||||  |
Db   4391 CACAGGTGCTCAGAAATCCTCGCCGAAGAAACTGGAACTCGACGAGACCTAGAAGACCAA 4450

Qy   1102 ccgctgactggagaagtgctaacctggttcactgacggaagcagctatgtggtggaaggt 1161
          ||  || | ||    |||| ||||||||  || ||||| ||||| |   |   |||||||
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Qy   1162 aagaggatggctggggcggcagtggtggacgggacccgcacgatctgggccagcagcctg 1221
          ||  |||  || |||||  |  | || || || |  || | || | ||||| |||||||||
Db   4508 AAACGGAGAGCAGGGGCCCCGATCGTAGATGGCAAGCGGACGGTATGGGCTAGCAGCCTG 4567

Qy   1222 ccggaaggaacttcagcgcaaaaggctgagctcatggccctcacgcaagctttgcggctg 1281
          || ||||| || ||||| || |||||||| ||  | ||| | ||||| || || || |||
Db   4568 CCAGAAGGTACGTCAGCCCAGAAGGCTGAACTAGTAGCCTTGACGCAGGCATTACGCCTG 4627

Qy   1282 gccgaagggaaatccataaacatttatacggacagcaggtatgcctttgcgactgcacac 1341
          |||||||| |||  ||| ||||| || ||||||||||||||||| |||||  ||||| || 
Db   4628 GCCGAAGGAAAAAACATCAACATCTACACGGACAGCAGGTATGCTTTTGCCACTGCTCAT 4687

Qy   1342 gtacacggggccatctataaacaaagggggttgcttacctcagcagggagggaaataaag 1401
           | || ||||| || ||||| || |||||| |||| || || || || || | || || || 
Db   4688 ATTCATGGGGCAATATATAAGCAGAGGGGGCTGCTCACTTCTGCTGGAAAAGATATCAAA 4747

Qy   1402 aacaaagaggaaattctaagcctattagaagccttacatttgccaaaaaggctagctatt 1461
          ||||||||||||||| |   |||  |||| ||| | ||| | || |   || | || |||
Db   4748 AACAAAGAGGAAATTTTGGCCCTGCTAGAGGCCATCCATCTCCCTAGGCGGGTCGCCATT 4807

Qy   1462 atacactgtcctggacatcagaaagccaaagatctcatatctagagggaaccagatggct 1521
          || ||||||||||| || ||||  |  |   | |   |  | |  ||||||| || ||| 
Db   4808 ATCCACTGTCCTGGCCACCAGAGGGGAAGTAACCCTGTGGCCACTGGGAACCGGAGGGCC 4867

Qy   1522 gaccgggttgccaagcaggcagcccaggctgttaaccttctgcctataatagaaacgccc 1581
          |||  || || ||||| || |||| | |    |   | || |   ||          |
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Qy   1582 aaagccccagaacccagacgacagtacaccctagaagactggcaagagataaaaaagata 1641
          ||| || ||  | |||  |||     | |   | |||||   |   |||  |
Db   4921 AAAACCTCAAGAGCCAATCGAGCCCGCTCAAGAAAAGACCAGGCCGAGGGAG-------- 4972

Qy   1642 gaccagttctctgagactccggaggggacctgctatacctcatatgggaaggaaatcctg 1701
                                                                   ||
Db   4973 ---------------------------------------------------------CTC 4975

Qy   1702 ccccacaaagaagggttagaatatgtccaacagatacatcgtctaaccacctaggaact 1761
           |||    |   ||   |||||   |  | | ||||||   |||| ||| ||||| | 
Db   4976 ACCCCTGACCGGGGAAAAGAATTCATTAAGCGGTTACATCAGTTAACTCACTTAGGACCA 5035

Qy   1762 aaacacctgcagcagttggtcagaacatccccttatcatgttctgaggctaccaggagtg 1821
           || | ||   ||  | || |      ||      |   | | ||  || | |      
Db   5036 GAAAAGCTTCTCCAACTAGTGAACCGTACCAGCCTCCTCATCCCGAACCTCCAATCTGCA 5095

Qy   1822 gctgactcggtggtcaaacattgtgtgccctgccagctggttaatgctaatccttccaga 1881
          | |  |   ||   ||  || |||  | | ||     ||  ||||||     |  ||   
Db   5096 GTTCGCGAAGTCACCAGTCAGTGTCAGGCTTGTGCCATGACTAATGCGGTCACCACCTAC 5155

Qy   1882 atacctccaggaaagagactaaggggaagccacccaggcgctcactgggaagtggacttc 1941
          | |    | ||||| || | | | |||   |  || ||||   ||||||| || ||||||
Db   5156 AGAGAGACCGGAAAAAGGCAACGAGGAGATCGACCCGGCGTGTACTGGGAGGTAGACTTC 5215

Qy   1942 actgaggtaaagccggctaaatacggaaacaaatatctattggtttttgtagacaccttt 2001
          || ||  ||||||| | |   || |||||||| ||||| || | || ||  ||||| || || 
Db   5216 ACAGAAATAAAGCCTGGTCGGTATGGAAACAAGTATCTGTTAGTATTCATAGATACTTTC 5275

Qy   2002 tcaggatgggtagaggcttatcctactaagaaagagacttcaaccgtggtggctaagaaa 2061
          || ||||||||||||| |||| |||||| || |  || ||  |     | ||   ||| |||
Db   5276 TCCGGATGGGTAGAAGCTTTTCCTACCAAAACTGAAACGGCCCTAATCGTCTGTAAAAAA 5335

Qy   2062 atactggaggaaatttttccaagatttggaatacctaaggtaatagggtcagacaatggt 2121
          ||| | || |||||| | ||  | || || || ||||||| || | ||||||||||||||| 
Db   5336 ATATTAGAAGAAATTCTACCCCGCTTCGGGATCCCTAAGGTACTCGGGTCAGACAATGGC 5395

Qy   2122 ccagctttcgttgcccaggtaagtcagggactggccaagatattggggattgattggaaa 2181
          || || || ||||| ||||||||||||||||||||||||||||   | |||||||  ||||||| 
Db   5396 CCGGCCTTTGTTGCTCAGGTAAGTCAGGGACTGGCCACTCAACTGGGGATAAATTGGAAG 5455

Qy   2182 ctgcattgtgcatacagaccccaaagctcaggacaggtagagaggatgaatagaaccatt 2241
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Db   5456 TTACATTGTGCGTATAGACCCCAGAGCTCAGGTCAGGTAGAAAGAATGAACAGAACAATT 5515
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Qy  2242 aaagagacccttaccaaattgaccacagagactggatgattgattggatggctctcctg 2301
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Db  5516 AAAGAGACCTTGACCAAATTAGCCTTAGAGACGGTGGAAAAGACTGGGTGACCCTCCTT 5575

Qy  2302 cccttgttgcttttaggtgaggaacacccctggacagtttgggctgaccccctatgaa 2361
         ||| | | |||||| ||| | ||||| |||  ||    |||  ||| ||| ||||||||
Db  5576 CCCTTAGCGCTGCTTAGGGCGCCAGGAAATACCCCTCGGCCGGGTTTGGTTTAACTCCTTATGAA 5635

Qy  2362 ttgctctacggggggaccccccccgttgggcagaaattgccttgcacatagtgctgatgtg 2421
         |||| ||| | | |||||| ||||| | ||| |||||| || ||||| |||| |||| |
Db  5636 ATTCTCTAPGGAGGACCACCCCCCCATACTTGAGTGTCTGGAGAAAACTTTTGGGTCCGATGAT 5695

Qy  2422 ctgcttcccagccctttgttcctctaggctcaaggcgctcgagtgggtgaggcagcgagcg 2481
         ||| | ||||| |||| || || |||| ||  ||   || || ||| | |||| ||||| |
Db  5696 AGATTTCTCCCTGTCTTATTTTACTCACTTAAAGGCTTTAGAAATTGTAAGGACCCAAATC 5755

Qy  2482 tggaggcaagctccgggaggcctactcaggaggagaacttgcaagttccacatcgcttccaa 2541
         |||| | |||||| |||||| || | |||| ||||| || |||| || ||| ||||||||||
Db  5756 TGGGACCAGATCAAAAGAGGTGTATAAGCCGGGTACCGTAACAATCCCTCACCGGTTCCAG 5815

Qy  2542 gttggagattcaagtctatgttagagcgccaccgtgcgaggaaacctcgagactcggtgggaag 2601
         |||| ||| || || || ||  ||| || ||| |||| ||| ||| ||| |   ||| ||||||
Db  5816 GTCGGGGGATCAAGTGCTTGTGCAGAGCCCATCGACCCAGCCCTTGAGCCTCGGTGGAAA 5875

Qy  2602 ggaccttatctcgtactttttgaccacacacaacggctgtgaaagtcgaaggaatcccccacc 2661
         ||  || | || || | |||| || |||| || ||| || ||| |||| |||| ||| ||||
Db  5876 GGCCCATACCTGGTGTTGCTTGGACTACCCCGCACCGGGTAAAAGTCGGATGGTATTGGTTGCC 5935

Qy  2662 tggatccaatgcaatcccaacgttaagccggggcgccacct------ccgattcggggtgggaaa 2715
         ||| |||||||   || ||| || ||||| || ||||| |      || || || ||||||
Db  5936 TGGGTCCAATGCTTCTCACCTCAAACCTGCACCACCTTCGGCACCACAGATGAGTCCTGGGAG 5995

Qy  2716 gccgaaaagcactgaaaatccccttaagcttcgcctccaatcggcggttgttcctttactctgtc 2775
         ||| ||||| |||| || |||||||||||| | |   | || ||||| |   || ||||
Db  5996 CTGGAAAAGACTGATCANTCCTCTTAAGCTCGCGTATTCGGCGGGCGGGGCGGGGACGAGTCTGCA 6055

Qy  2776 aa 2777
         ||
Db  6056 AA 6057
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Query Match   28.1%;  Score 933.6;  DB 1;  Length 8323;
Best Local Similarity   60.0%;  Pred. No. 3.3e-274;
Matches 1702;  Conservative 0;  Mismatches 1094;  Indels 42;  Gaps 7;

Qy   19 acagatgccttcttcctgcctgagattacacccactagccaaccacttttgccttcgaa 78
         |||||| || ||||| ||||||| ||| || ||| ||||| || || |||| || ||||
Db 3049 AAAGATGCTTTTTTTCTGCCTGGATCCACCCACCCAGTCAGTCGTCTCTTGCGCTTTGAG 3108

Qy   79 tggaggagatccaggtacgggaagaaccgggcagctcaacctgacccgactgcccaggg 138
         ||| | |||||||| || |||||| || |||||| || |||  ||| | ||| || |||||
Db 3109 TGGACAGGATCCAGAAGATGGGAAATCTCAGCACACACAATTAAACCTGGACAGACTCCCCGCCAGGGT 3168

Qy  139 ttcaagaaatccccgggaccacatctttgacgagaagccttacacacaaggggaccttcagg 198
         |||||   ||| | |  ||||| || |||| || ||||| || |||  |||| ||| ||  |||
Db 3169 TTCAAAAACAGTCCCACCCTGTTTCAGTGAAGCCCTGCACAGGGACCTCGCAGACTTCCGG 3228

Qy  199 atccaacaccctcaggtgaccctcctccagtacggtggatgacctgctttctgggggagc 258
         ||||| ||||| || |||| | ||| |||||| | |  | |||| || |||| || ||||
Db 3229 ATCCAGCACCCCAGACCTGAATTCTCCAGTATTGTAGAGTACTTACTGGTGGCCGCCACT 3288

Qy  259 accaaacaggactgcttagaagtacgaaggcactactgctggaaattgtctgacctaggc 318
         | |||||||||| |||||| || ||| |||| |||| ||||| |||| |||| ||| |||
Db 3289 TCTGAGCTTGACTGTCAACAAGGTACGCGCGGGCCCCTGTTACAAAACCCTAGGGACCTCGGA 3348

Qy  319 tacagagccctgctctaagaaggcccagatttgcaggaggaggaggtaacatacttgggttac 378
         || | |||||| || ||||||| || |||||||| ||| |  |||| |||| ||||||| |||
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Qy  379 agtttcgcgggcgggggacggatggtggtggctgacggaggcacggagaaaaaacttgtccaagata 438
         || ||| | ||| | || ||  ||| ||| ||||| || ||| ||| |||||| || | |||||
Db 3409 CTTTCTAAAAGAGGGTGCAGAGATGGGTGACTGAGCGCCAGAAAAAGAGACTGTGATGGGGCAG 3468

Qy  439 ccgggcccaaccacagccaaacaagtgagagagtttttgggggacagctggattttgcaga 498
         || || |||||| ||||||||| ||||| |||||||| ||||| ||||||| ||||| |||
Db 3469 CCTACTCCGAAGACCCTCGACAAACTAAGGGAGTTCCTAGGGACCGGCAGGCTTCGTCGTCGC 3528

Qy  499 ctgtggatcccgggggttttggcgacctagcagccccaacctctaccccgctaaccaaagaaaaa 558
         || |||||||| ||||||||| | |||||||||||||||| ||||| ||||| ||||| ||| |
Db 3529 CTCTGGATCCCTGGGGTTTGCAGAAAATGGCAGCCCCCCTTGTPACCCTCTCACCAAAACGGGG 3588

Qy  559 gggggattctcctgggcgtcctgaccaccagaaggcacattgatgctatcaaaaaggccctg 618
         ||||| |||||||||| || |||||| ||||| ||||| ||||| ||||||||  |||||||
Db 3589 ACTCTGTTTTGAGTGGGGCCCCAGAACCAGCAAAAAGGCCTACCAAGAGAATCAAGCAGGCTCTC 3648

Qy  619 ctggagcgcaactcgctcctgccctccctgacgtaactaaacccttacccttttatgtggat 678
         |||||| | |||| | | ||||||||| || | |||||||||||  ||| |||||| || ||
Db 3649 TTAACTCCCCCTGCCCTGGATTGCCAGACTTGACTTAAGCCCTTCGAACTTTTTGTTGAC 3708

Qy  679 gagcgtaagggagtagcccgggaggagttttaacccaaacccttaggagaccatggaggagacct 738
         ||| | || || || ||| ||||| || || ||||||| || || ||  |||| ||| |||||
Db 3709 GAGAACGACAGGGCTACGGCCAAGGTGTCCTAACGCAAAAACTGGGGGCCTTGGCGTCGGCG 3768

Qy  739 gttgcctacctgtcaaagaagagttgatcctgtagcccagtgttgggccgtatgtctgaag 798
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Db 3769 GTGGCCTCACCGTCCAAAAAGCTAGACCCAGTGGCAGCTGGGTGGCCCCCTTGCCTACGG 3828

Qy  799 gctatccgcagctgtgggccatactggtcaaggacgcgtgacaaaattgacttggggacgaat 858
         |||| | ||| |   ||| |||| ||||||||| |||||| | ||  | | || || ||||||
Db 3829 ATGGTAGCAGCCATCGCCGTTCTGACCAAAGACGCGTTGGCAAGCTCACCATGGACAGCCCA 3888

Qy  859 ataactgtaatagccccccatgcattggagagaacatcgttcggcagccccccagaaccgatgg 918
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